

FIGURE 1

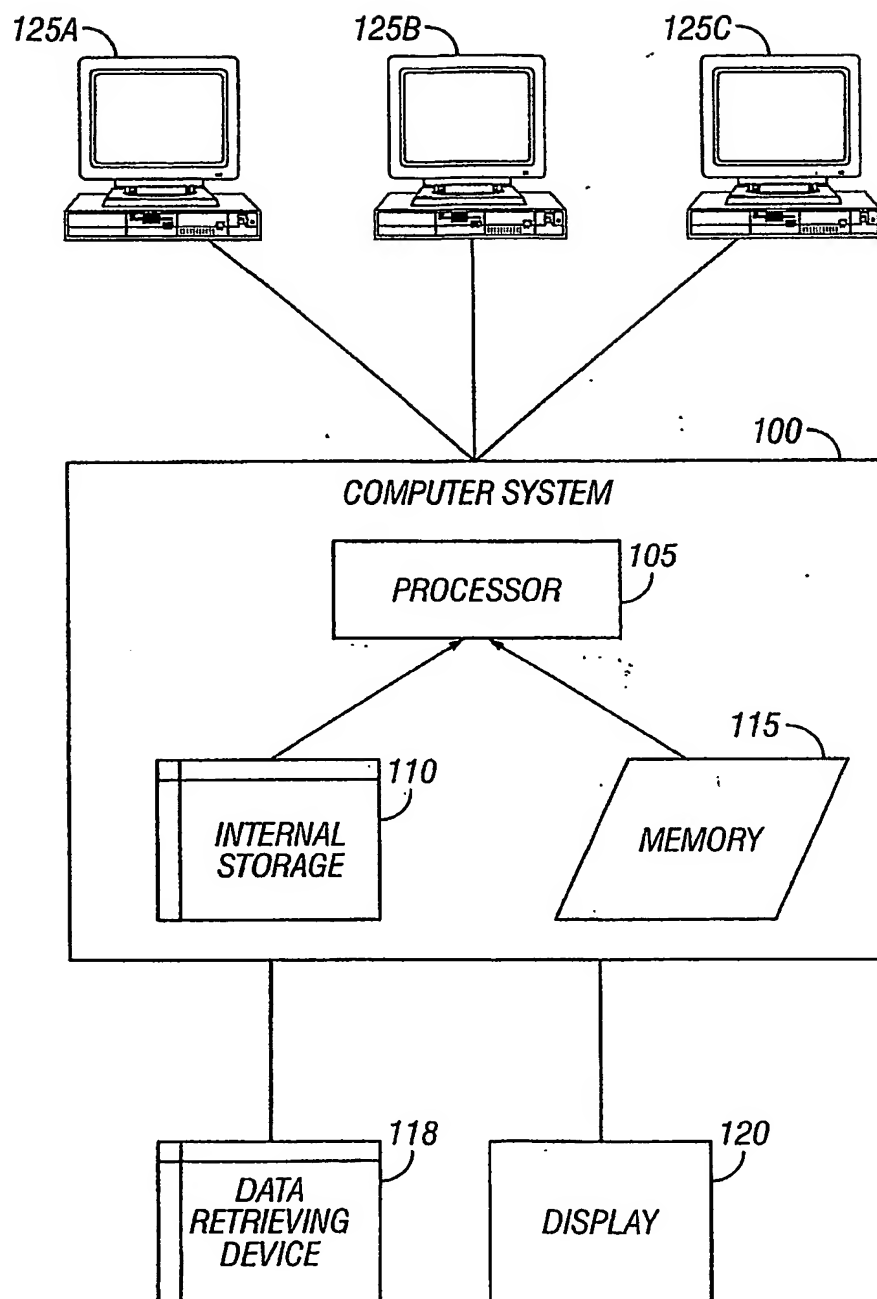


FIGURE 2

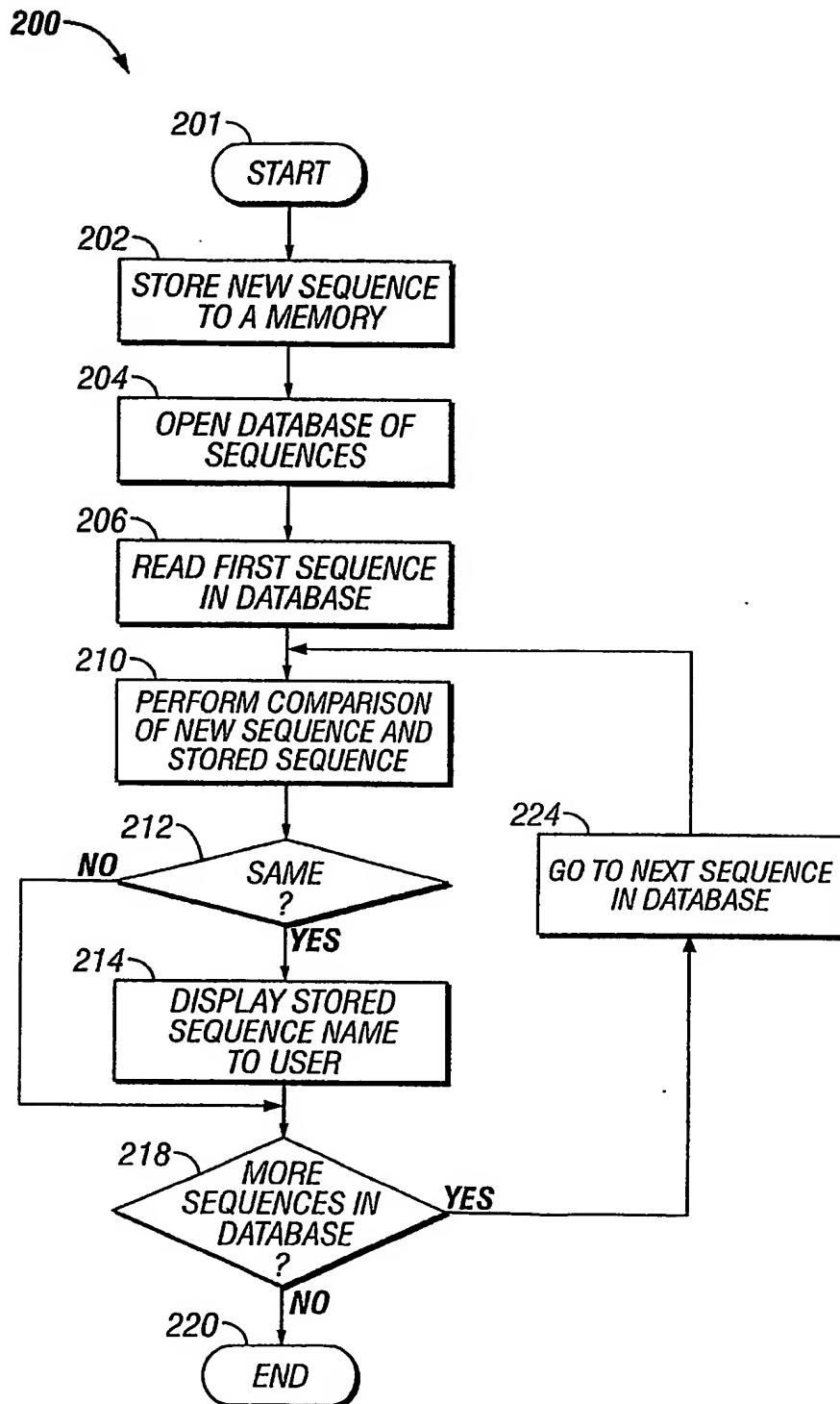


FIGURE 3

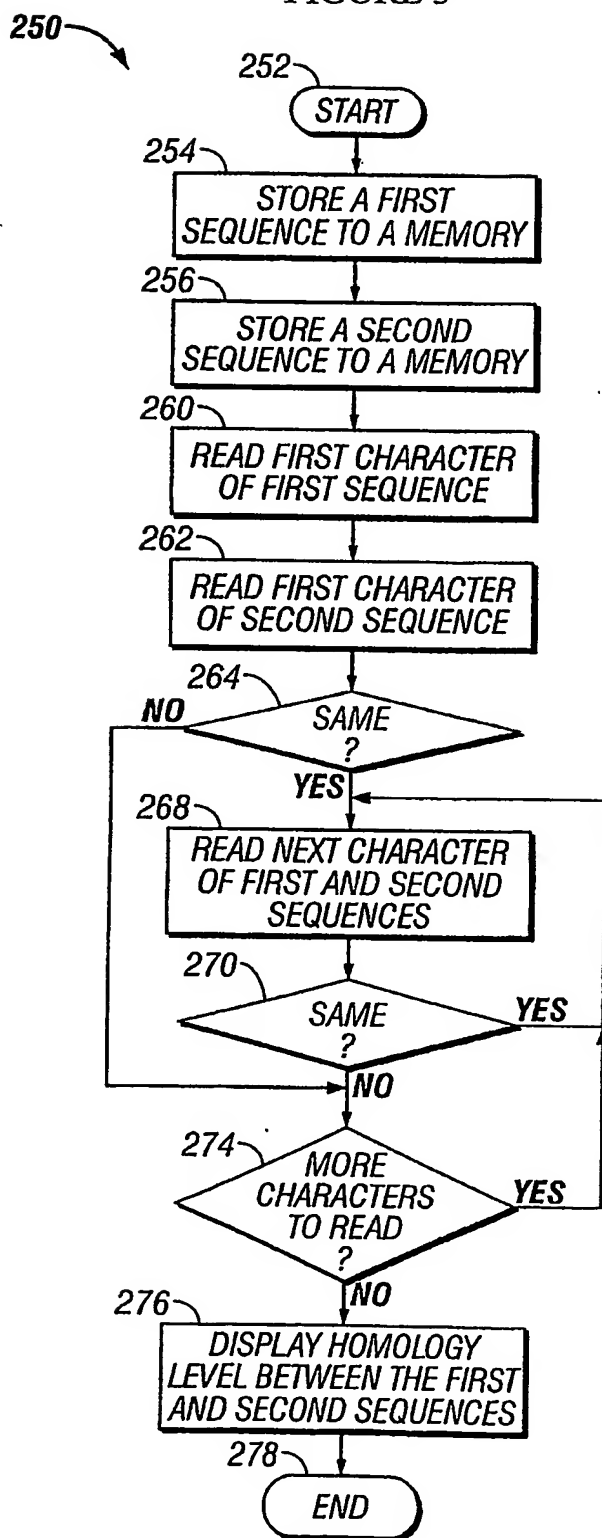


FIGURE 4

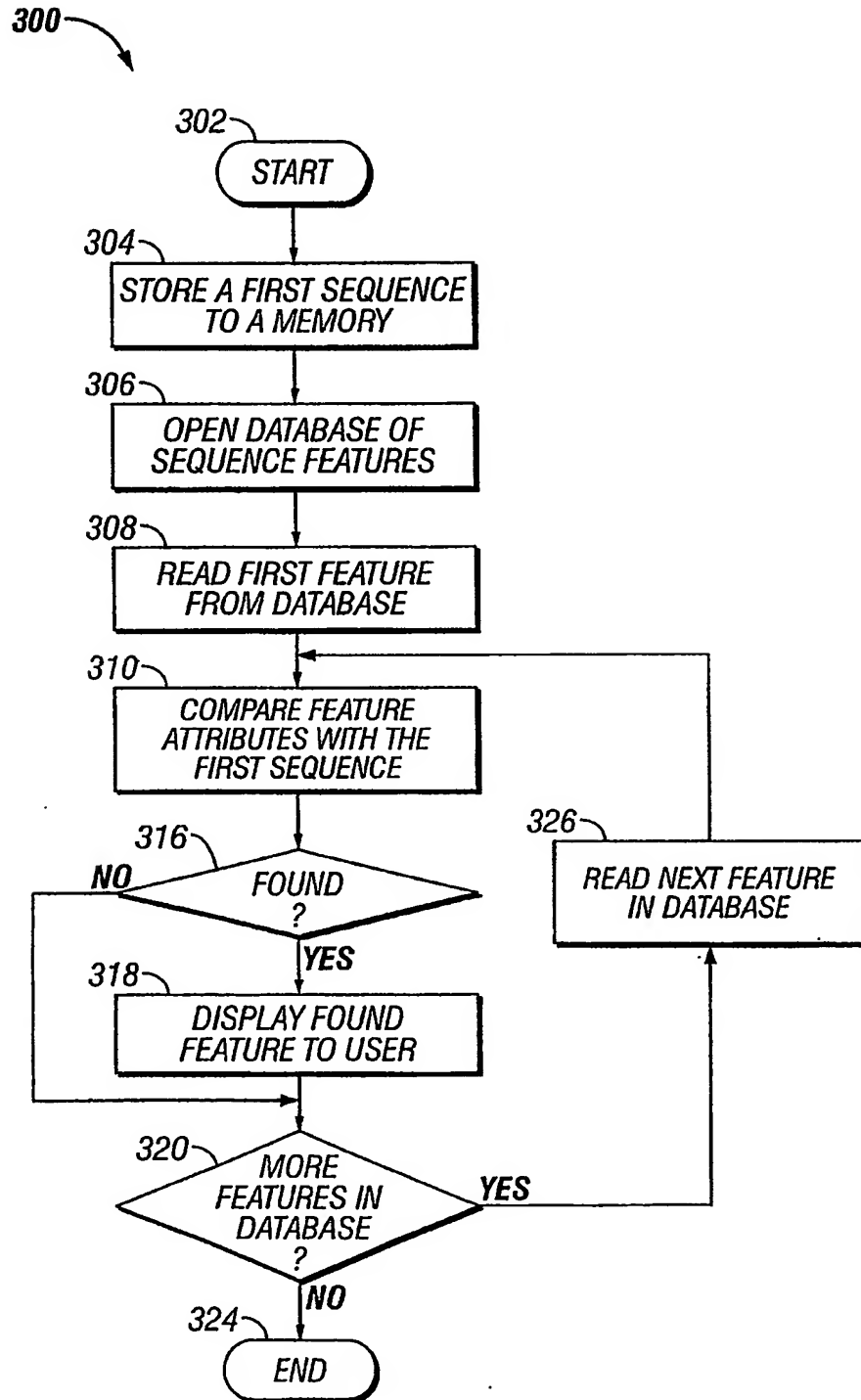


FIGURE 5

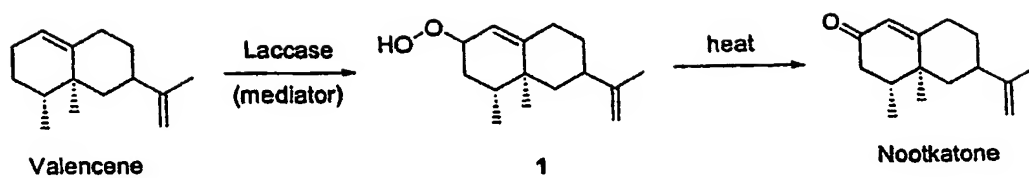


FIGURE 6

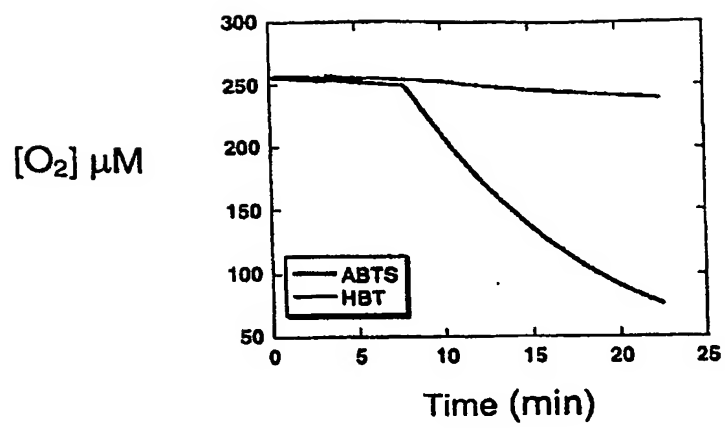


FIGURE 7

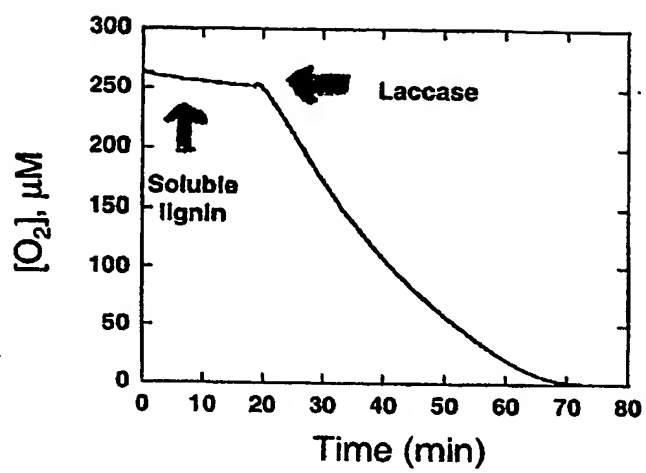


FIGURE 8

Enzyme, 57 mU	ABTS	HBT			TEMPO	Lignin, pH 9 (4 mg/ml)
		pH 5	pH 7	pH 9		
<i>T. versicolor</i>	16.5	0.52	0.08	0 ²	0 ²	-
<i>P. ostreatus</i>	19	-	-	0.8 ²	3.0 ²	7.45 ²
SEQ ID NOS:15, 16 (expressed in <i>Pichia</i>)	17.4	0.15	0	0	0.8 ²	6.2 ± 2.4
SEQ ID NOS:15, 16 ¹	15	TBD	0.32	0.57	12.6 ²	20 ± 0.35
SEQ ID NOS:9, 10 ¹	14.2	TBD	TBD	TBD	TBD	
SEQ ID NOS:5, 6 ¹	3.6	0.37	0.1	0.1	0.31 ²	0
SEQ ID NOS:13, 14 ¹ (expressed in <i>Pichia</i>)	8 ³	0	0.06	0	TBD	6
SEQ ID NOS:13, 14 ¹	10.8 ³	0.16 ³	0.29	0.3	1.4 ²	1.8
SEQ ID NOS:19, 20	5.7	0		0.08		

¹includes 100 μ M CuSO₄; ²0.3 U enzyme; ³pH 6

FIGURE 9

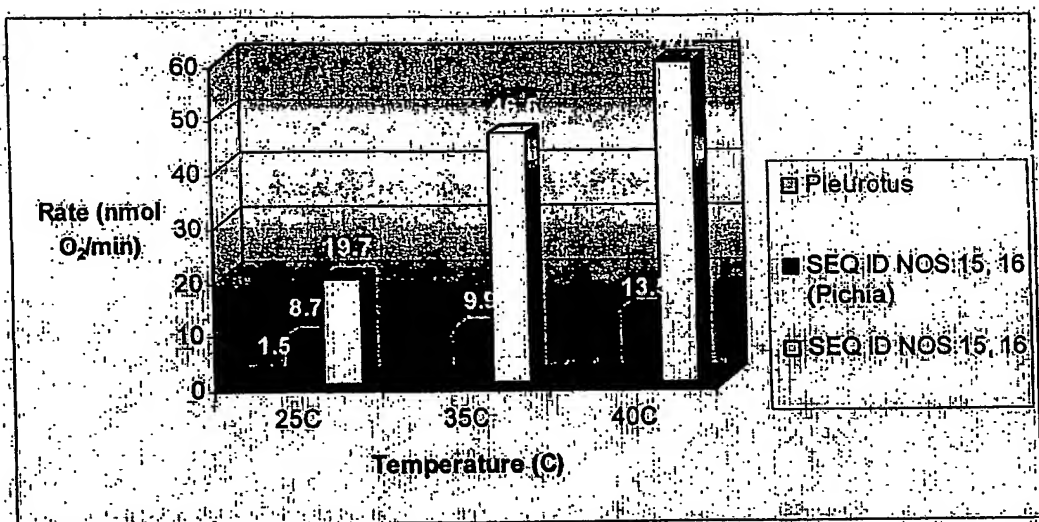


FIGURE 10

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      10      20      30      40      50      60
SEQ ID NO:4 MLRPEDATRRRAFIHAATMSCLVAAGASGLTLTREVRAGFRANFQFIPDLEIQLNAREDH 60
SEQ ID NO:8 -MDGFVESRRREFIRTTGMT-----AGAMFSSQNLEFAAAABAAADYT-----VRIKA--AP 48
Consensus   :      ** **:: * :      * : : : * \ * : :      : : : * 27

      70      80      90      100     110     120
SEQ ID NO:4 VSIPLGPLTRVWRVDGKVKVKGDPGNLAFLSNGYLEVVRVRRCOKVRIDEVNQLAEFTIIF 120
SEQ ID NO:8 IETASDKILSTITYNGQFPG-----PLIRLKECROVTVDIENETDTEQOLH 94
Consensus   : : * . . : . : * : : :      * : : : : : : * : : * : * 52

      130     140     150     160     170     180
SEQ ID NO:4 WHGLYVPAAMDGHPRN-----AVSTGEHYVYEFETIANQAGTYWEHAHPDGRRTGAQIYFGLA 176
SEQ ID NO:8 WHGQFVSPDVDCAAEEGTPIYPAHCORRIMFTPGPAGLRFYHTHNRAQADLSLGQYSGQV 154
Consensus   *** : : . : * : : :      : * : : :      * * : . . :      * * . 71

      190     200     210     220     230     240
SEQ ID NO:4 CVLIVDDEEAAAGLPFGPYDVPLVIQDRITFDDRNQFTYLAEGNEGMMGMMGNGGMMGRG 236
SEQ ID NO:8 GPVYIEPKENECRYDREVFLLKEFEP--ILSRGGDMPEQDFLSPSAIDKTLKETCEAAMKA 213
Consensus   * : : : * . . : : * : : : : : : . . : : : * : : : 89

      250     260     270     280     290     300
SEQ ID NO:4 GMMGGGGMGOMMARMMGFLGDRIIVNGKEDFVLPVAARAYRLRLNGSNTRIYKLAWSDR 296
SEQ ID NO:8 SLAKRMPHGYEVGKYKFTTINGRMIGHGEE--IRVKHGERVLFHILNGSATETIRSLALPDH 271
Consensus   : :      * : . : : : * : * : :      : : : * * * * * : * : : 115

      310     320     330     340     350     360
SEQ ID NO:4 TPLTVICTDGGLLERPVTRQYVTLAPAERVDVWVDFSRWPGTKLTLOS-LAFDGVLAGM 355
SEQ ID NO:8 S-FEVIALDGNPVPNPVHPVPLWLGTAERTSAVVEMNHPGWILGDLADDDRNHGMGVV 330
Consensus   : : * : . * : : * : : : * : : : : * : : : : * : : : 139

      370     380     390     400     410     420
SEQ ID NO:4 GMIGNTSLESGASEFVLKVGVVDQRANTKMBLEARLASLPPVRFQDAVNAHNPKVENITMG 415
SEQ ID NO:8 EYAGRSCKPHWATFPFPRWDYARFAKENASAE-----EADAEADMTFAKDNAAEAC 381
Consensus   * : . : * : * : : : : : : : * : : : : * : : : * 158

      430     440     450     460     470     480
SEQ ID NO:4 MMVHGVNCRRFEMNCVAKTETVRRNSTEIWEEFNESMMLMAHSMHVEGLQFRVLERTVQ 475
SEQ ID NO:8 FNRWTINGVAYPMSNEMAPASEHLROGKRYILMRN-ASDDIIFIHLRHSEFLAN----- 436
Consensus   : * : * : : * : : : : : : : : : * : : * : : : 180

      490     500     510     520     530     540
SEQ ID NO:4 PDFRAGYRTLAAGLVDDGWKDTVLLMPCERIRLLLRFASTGLFLYHCFMLEHEDSGLMR 535
SEQ ID NO:8 -----LACTKTAGVMKDVMMLGGYQOLEIDFVADNPGTLFLHCHQOLEMDRGFMA 486
Consensus   : : : * : : : : : : : : * : * * * * * * * : * : 203

      . . . . |
SEQ ID NO:4 NYLIQT 541
SEQ ID NO:8 LFDYV- 491
Consensus   :      204

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FIGURE 11A

	10	20	30	40	50	60	
SEQ ID NO:2	-----MTREKFVDALPIPDTLKPVQQSKDSTY-YEVTMEECYHQLHR-----	D	42			
SEQ ID NO:16	-----MTLEKFVDALPIPDTLKPVQQSKDSTY-YEVTMEECYHQLHR-----	D	42			
SEQ ID NO:18	-----MDVGGPVD-----Y-YEIAVRQFQQQILPP-----	P	25			
SEQ ID NO:20	MTTRRDFLKRAGLGLAAAATLPVLSGCPDALFRYGVATRRSADGLLDTRLRLRFSHTCIG	60				
SEQ ID NO:26	-----MATVPATTREFPAALG-----TGRDSP-----	21				
SEQ ID NO:14	---MTAAGAALTASGLISRTSLSDTRAGGPAGASPFAPVAAQALAP-----	IV	48			
SEQ ID NO:6	-----MDRRKFIKTSLFSALGFSVGGLSLLSCGGGGTTGSSSGQSG-----	42				
Consensus							1
	70	80	90	100	110	120	
SEQ ID NO:2	LPPTRLWGYNG-----LFPGPTIKAKRNENVYVKWMNNLPS-----	EHFLPIDHTI	88			
SEQ ID NO:16	LPPTRLWGYNG-----LFPGPTIKAKRNENVYVKWMNNLPS-----	EHFLPIDHTI	88			
SEQ ID NO:18	LPATTVWSYSGSTNHSGETFNYPATFIEAKWNTPVRVKWINDLKDLSSGEFLPHLLPVDPTL	85				
SEQ ID NO:20	HEQVYTRAYDG-----RIPGPVLRVKPGDTLKIIRLINDLPDE-----	E---DGH	101			
SEQ ID NO:26	-----VISGLAD-----		28			
SEQ ID NO:14	TPFRTAMPIPP-----VARPVSVTSTTDYSIPVTQTAEIIPG-----	VRTPVL	93			
SEQ ID NO:6	TLKQSLNIPG-----YFLFPDQQRVSITAKWTTLEVIPGKST-----	DMLVYEIDN	89			
Consensus							1
	130	140	150	160	170	180	
SEQ ID NO:2	HHSDS-----QHAPEVKT-----VVHLHGGVTPDDSDGYPEAWFS-----	124				
SEQ ID NO:16	HHSDS-----QHAPEVKT-----VVHLHGGVTPDDSDGYPEAWFS-----	124				
SEQ ID NO:18	HWANPPGGLGGROMRPEFTTTPDYRGVPVIVTHLHGGHTSQESDGFTEAWYLPATNIP	145				
SEQ ID NO:20	GHAKS-----DDVNVPHGFN-----TTNIHTHGLHVSPSGNSDNVFN-----	138				
SEQ ID NO:26	-----VTNLHTHGFHVSPSGNSDNIFL-----	50				
SEQ ID NO:14	TYGGSFPGPTIKARSGRRVVVKQPNRITTTGSMHLHGAVVDPANDGGEMLIT-----	146				
SEQ ID NO:6	EYNPVI FLRKQTF SADFVNNSGED-----SIHWHGFRAPWKS DGH EYAVK-----	137				
Consensus							3
	190	200	210	220	230	240	
SEQ ID NO:2	KDFEQTGPYFK-----REVYHYENQORGAILWYHDHAMAALTRLNVYAG	167				
SEQ ID NO:16	KDFEQTGPYFK-----REVYHYENQORGAILWYHDHAMAALTRLNVYAG	167				
SEQ ID NO:18	AGFATEGTWYDTFKTQFLNQWGVWPQPGSAIFQYANDQRASTLWYHDHALGMTRLNVYAG	205				
SEQ ID NO:20	Q--IPPETHFD-----YEYNIPANHPAGTFYHHPHKHGSVTNQMMGG	178				
SEQ ID NO:26	H--INPGTFD-----YEFKLPANHSPGMYWYHHPHGHGDTAPQCNGG	90				
SEQ ID NO:14	PGQRT-----EVEGIAGL--TERLLVLQATQFDGDN-----	127				
SEQ ID NO:6	-----DGETYS-----YTPENPQVAATLWYHDHAHMEAEHVYRG	181				
Consensus							10
	250	260	270	280	290	300	
SEQ ID NO:2	LICAYIIHEPKE-----KRLKLPESGE-----YDVPLLITDRTINEDGSLFYPSG-	211				
SEQ ID NO:16	LICAYIIHEPKE-----KRLKLPESGE-----YDVPLLITDRTINEDGSLFYPSG-	211				
SEQ ID NO:18	PAGFYLLRGGPDDMVVGTLPGPAPALDDPSGMKY--YEIPLAIQDRSFNKGCSLFYPDSR	263				
SEQ ID NO:20	MAGALIVEGDID-----RVPEIAAA--KDYIFLLQELRFEEDGHAPA----	218				
SEQ ID NO:26	MAGVILIDGGLD-----EVEGIAGL--TERLLVLQATQFDGDN-----	127				
SEQ ID NO:14	MSGFYLISSDNE-----DALPLERGT-----YDVPIVVRDIGLNPDTLFFDHN-	225				
SEQ ID NO:6	LACMIIIEDEDE-----DNLKQALDLEYGVIDIPLIQDKTFDSSGQLVYN--	219				
Consensus							20
	310	320	330	340	350	360	
SEQ ID NO:2	---PENPSPSLPN---PSIVPAFCGDTILVNGKAWPYMEVEP-RKYRFRVINASNTRTY	263				
SEQ ID NO:16	---PENPSPSLPN---PSIVPAFCGDTILVNGKAWPYMEVEP-RKYRFRVINASNTRTY	263				
SEQ ID NO:18	RFFDGFKKAYIPDSDISPIWNPEFFGKVMVNVNGRSWFFLEVEP-RRYRFRLLNGCNSRFL	322				

FIGURE 11B

SEQ ID NO:20	----HFPFHDLDN-----LMLFR--TVNGQVNP	TIYLRPGEVQRWRFIHAGVEHYL	263
SEQ ID NO:26	----LVPYNNQSN-----ATRQR--EVNGQLNP	TIYLRPGEVQRWRFIHAGVEHYL	172
SEQ ID NO:14	-----FDTRPQ-----	ILVNGKPOPYFQVAA-RKYRLRLILNGSNQRP	262
SEQ ID NO:6	-----PMGHMG-----	FWGDTILVNLTPNPYMDVER-KIYRFRIILNGSNARPY	261
Consensus		** * : : * * : : *	28
	370 380 390 400 410 420		
SEQ ID NO:2	NLSLDN-G--GEFIQIGSDGGLLPRSVKLSNFSIAPAE	RFDILIDFAAFE-GQSIILANS	319
SEQ ID NO:16	NLSLDN-G--GEFIQIGSDGGLLPRSVMLNSFSIAPAE	RFDILIDFAAFE-GQSIILANS	319
SEQ ID NO:18	ILKFSNPN--LSFWQIGNDGGFLPAPVQLSOLLMSPAER	ADIVDFSQFTPGTEIILENT	380
SEQ ID NO:20	PLELDG---HSLHQIAQDGIARFSPPEETDSVFLTPGN	RADVLRGG-QP-GTYILRKQA	317
SEQ ID NO:26	LLALAG---HTLHQIAADGNPYDEVVPRDQILLP	PSERVEVLVQASTQL-GSYEFRTLL	227
SEQ ID NO:14	EFRLSD-G--GEFTQIASDRGLLPAPYTTTTLPLSPA	ERADIVDFSRYPVGSVVLENA	319
SEQ ID NO:6	RLALLRGNQRMRFVVLGVGGLLDTPKEVNEILVAP	GERIDILVDFRDASVNDVIKLYNF	321
Consensus	: : : * : : . : * : * : : : .		41
	430 440 450 460 470 480		
SEQ ID NO:2	-----EGCGG-----	DVNPETDANIMOFRVTK-PLAQKDES	351
SEQ ID NO:16	-----EGCGG-----	DVNPETDANIMOFRVTK-PLAQKDES	351
SEQ ID NO:18	GP-----	DEPFGGGEPSDFSADAKDTTRQVMQFRVV--PLTTADT	422
SEQ ID NO:20	-----YDQ-----	GRGEVPEDIIATVVVGGPPSFMRLPWLL	348
SEQ ID NO:26	-----WGD-----	DFQAEPDVVLATMVVAG---EAITPAPL	255
SEQ ID NO:14	-----	YFPEPSNKEILRFDDVVR---SAYDPSSV	344
SEQ ID NO:6	PHNLIGMGMIGMRMGMERGMGMNGMNMMDGMADN	SEFEVMEFRVTK--DSAYDKSIP	379
Consensus		: : * :	43
	490 500 510 520 530 540		
SEQ ID NO:2	PKYLASYPSVRHERIQNLRLTKLAG--TQDQYG--	RPVLL--LNN-----KRWHDPVT	398
SEQ ID NO:16	PKYLASYPSVQHERIQNLRLTKLAG--TQDQYG--	RPVLL--LNN-----KRWHDPVT	398
SEQ ID NO:18	PNLLELPATGLGAATNRQVSLNEEDSAVLFGVG	PRAALLGTLDSERGEPEIRGWDDAIT	482
SEQ ID NO:20	PTPAL-HRTITDEEVTSRSIVFSV--QPAPAG--	EMFPRFLIDG-----HTFSPDRVD	397
SEQ ID NO:26	PTALIPYEDLRDVPVDNIRVTFTEE--PGAP--	L--YLAIDG-----KHFDPRVD	300
SEQ ID NO:14	PARLATLPPTAAPTQTRNYTLDFDVQTGAGS--	IS-----G-----KTWDEQRVD	387
SEQ ID NO:6	QRLSEVTPINTDGAQVQRITLGMRRMVFTIN--	GETWEDGYANP---QDINNPKVL	430
Consensus		: : : : *	45
	550 560 570 580 590 600		
SEQ ID NO:2	EAPKAGSTEIWSIINPT-RGTHPIHLVLSFRVLD	RRPFDARFEERGEAYTGFAVPPP	457
SEQ ID NO:16	EAPKAGSTEIWSIINPT-RGTHPIHLVLSFRVLD	RRPFDARFEERGEAYTGFAVPPP	457
SEQ ID NO:18	ENPALGSIEVWEIHNT-EDAHPIHIEVAFEVVNR	QPFEGS---ARG-----PE	528
SEQ ID NO:20	HSIPLCSVEEWTVINNH-REDHPFHIEVNAFEV	THLNGDRLP-----	438
SEQ ID NO:26	QTVKLGAEEWIVRNTS-SEWHPFHIEVNDFO	VIANNNEAVN-----	341
SEQ ID NO:14	TTVRQGDTEVWEIKNTHPFIPHNEHIELVDF	RILOIDGKPPT-----PG	431
SEQ ID NO:6	EEQNNGDVIIEYVNT-GMYHPMTHGFOFQV	FLERSLGLR-----	471
Consensus	* * * : * : : : *		54
	610 620 630 640 650 660		
SEQ ID NO:2	PSEKGWKDTVQSHAGEVLRITAVTFGP-YTG--	RYVWHCHILEHEDYDMRPMDDVIDPHKS	514
SEQ ID NO:16	PSEKGWKDTVQSHAGEVLRITAVTFGP-YTG--	RYVWHCHILEHEDYDMRPMDDVIDPHK	513
SEQ ID NO:18	VWEGGFKDTVIAYPEEITRVKAHFD--LPG--	LYVWHCHIVEHEDNEMRPY-FIGP--	580
SEQ ID NO:20	--RPRWHDVINVPFGTATFTRTFED-FTG--	KFVLHCHLLVHEDLGMOTVEVT----	488
SEQ ID NO:26	--THGYEDSVALPPHSETTMRMKFLD-FSG--	KFVYHCHILGHEDFGMAVVEVVE----	392
SEQ ID NO:14	--DAGLKDTVIRIGGETARILVHFDFPYSG--	RYYYHCHLIDHSSMGMMANLEITR----	483
SEQ ID NO:6	ATDLGWKDTVIVARMETVRIVAVMSHPYNEHQ	IYLLHCHILEHDEGMMVNYRVNA----	527
Consensus	* : : : : * : : * : *		66

FIGURE 12

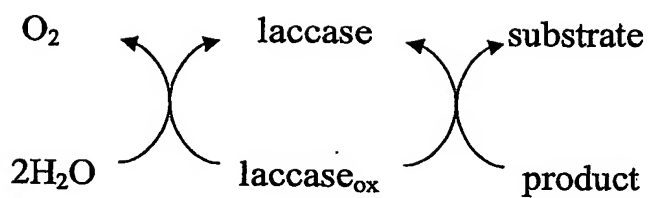


Figure 12B

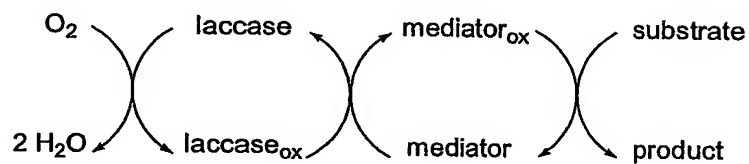


Figure 12C

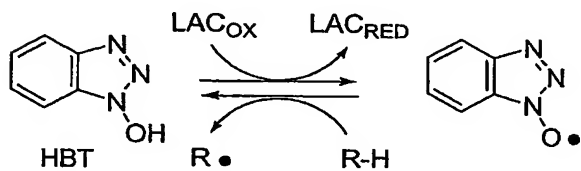


Figure 12D

